

**SEQUENCE LISTING**

<110> Scadden, David T.  
Poznansky, Mark C.  
Olszak, Ivona T.  
Brown, Edward M.

<120> THE CaR RECEPTOR AS A MEDIATOR OF MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS

<130> M0765/7038/ERG/KA

<150> PCT/US00/15440  
<151> 2000-06-02

<160> 2

<170> FastSEQ for Windows Version 3.0

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<213> Homo

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<223> Ca-sensing Receptor

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gtc ctc ttg gca ctc acc tgg cac acc tct gcc tac ggg cca gac cag 100  
 Val Leu Leu Ala Leu Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln  
     10             15             20

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cga gcc caa aag aag ggg gac att atc ctt ggg ggg ctc ttt cct att      148
Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile
   25           30           35           40
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cat ttt gga gta gca gct aaa gat caa gat ctc aaa tca agg ccg gag 196  
 His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu  
                   45                  50                  55

tct gtg gaa tgt atc agg tat aat ttc cgt ggg ttt cgc tgg tta cag 244  
 Ser Val Glu Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln  
               60                  65                  70

gct atg ata ttt gcc ata gag gag ata aac agc agc cca gcc ctt ctt 292  
 Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu  
                  75                 80                 85

ccc aac ttg acg ctg gga tac agg ata ttt gac act tgc aac acc gtt 340  
 Pro Asn Leu Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val  
           90             95             100

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Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile
105          110          115          120
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gat tct ttg aac ctt gat gag ttc tgc aac tgc tca gag cac att ccc Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Glu His Ile Pro	436
125 130 135	
tct acg att gct gtg gtg gga gca act ggc tca ggc gtc tcc acg gca Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Val Ser Thr Ala	484
140 145 150	
gtg gca aat ctg ctg ggg ctc ttc tac att ccc cag gtc agt tat gcc Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala	532
155 160 165	
tcc tcc agc aga ctc ctc agc aac aag aat caa ttc aag tct ttc ctc Ser Ser Arg Leu Leu Ser Asn Lys Asn Gln Phe Lys Ser Phe Leu	580
170 175 180	
cga acc atc ccc aat gat gag cac cag gcc act gcc atg gca gac atc Arg Thr Ile Pro Asn Asp Glu His Gln Ala Thr Ala Met Ala Asp Ile	628
185 190 195 200	
atc gag tat ttc cgc tgg aac tgg gtg ggc aca att gca gct gat gac Ile Glu Tyr Phe Arg Trp Asn Trp Val Gly Thr Ile Ala Ala Asp Asp	676
205 210 215	
gac tat ggg cg <sup>g</sup> ccg ggg att gag aaa ttc cga gag gaa gct gag gaa Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala Glu Glu	724
220 225 230	
agg gat atc tgc atc gac ttc agt gaa ctc atc tcc cag tac tct gat Arg Asp Ile Cys Ile Asp Phe Ser Glu Leu Ile Ser Gln Tyr Ser Asp	772
235 240 245	
gag gag gag atc cag cat gtg gta gag gtg att caa aat tcc acg gcc Glu Glu Glu Ile Gln His Val Val Glu Val Ile Gln Asn Ser Thr Ala	820
250 255 260	
aaa gtc atc gtg gtt ttc tcc agt ggc cca gat ctt gag ccc ctc atc Lys Val Ile Val Val Phe Ser Ser Gly Pro Asp Leu Glu Pro Leu Ile	868
265 270 275 280	
aag gag att gtc cgg cgc aat atc acg ggc aag atc tgg ctg gcc agc Lys Glu Ile Val Arg Arg Asn Ile Thr Gly Lys Ile Trp Leu Ala Ser	916
285 290 295	
gag gcc tgg gcc agc tcc tcc ctg atc gcc atg cct cag tac ttc cac Glu Ala Trp Ala Ser Ser Leu Ile Aia Met Pro Gln Tyr Phe His	964
300 305 310	
gtg gtt ggc ggc acc att gga ttc gct ctg aag gct ggg cag atc cca Val Val Gly Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly Gln Ile Pro	1012
315 320 325	
ggc ttc cgg gaa ttc ctg aag aag gtc cat ccc agg aag tct gtc cac Gly Phe Arg Glu Phe Leu Lys Lys Val His Pro Arg Lys Ser Val His	1060
330 335 340	
aat ggt ttt gcc aag gag ttt tgg gaa aca ttt aac tgc cac ctc Asn Gly Phe Ala Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys His Leu	1108
345 350 355 360	
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Gln	Glu	Gly	Ala	Lys	Gly	Pro	Leu	Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	
			365			370							375			
cac	gaa	gaa	agt	ggc	gac	agg	ttt	agc	aac	agc	tcg	aca	gcc	ttc	cga	1204
His	Glu	Glu	Ser	Gly	Asp	Arg	Phe	Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	
			380			385							390			
ccc	ctc	tgt	aca	ggg	gat	gag	aac	atc	agc	agt	gtc	gag	acc	cct	tac	1252
Pro	Leu	Cys	Thr	Gly	Asp	Glu	Asn	Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	
			395			400							405			
ata	gat	tac	acg	cat	tta	cg	ata	tcc	tac	aat	gtg	tac	tta	gca	gtc	1300
Ile	Asp	Tyr	Thr	His	Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	
			410			415							420			
tac	tcc	att	gcc	cac	gcc	ttg	caa	gat	ata	tat	acc	tgc	tta	cct	ggg	1348
Tyr	Ser	Ile	Ala	His	Ala	Leu	Gln	Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	
			425			430							435			440
aga	ggg	ctc	ttc	acc	aat	ggc	tcc	tgt	gca	gac	atc	aag	aaa	gtt	gag	1396
Arg	Gly	Leu	Phe	Thr	Asn	Gly	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	
			445			450							455			
gcg	tgg	cag	gtc	ctg	aag	cac	cta	cg	cat	cta	aac	ttt	aca	aac	aat	1444
Ala	Trp	Gln	Val	Leu	Lys	His	Leu	Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	
			460			465							470			
atg	ggg	gag	cag	gtg	acc	ttt	gat	gag	tgt	ggt	gac	ctg	gtg	ggg	aac	1492
Met	Gly	Glu	Gln	Val	Thr	Phe	Asp	Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	
			475			480							485			
tat	tcc	atc	atc	aac	tgg	cac	ctc	tcc	cca	gag	gat	ggc	tcc	atc	gtg	1540
Tyr	Ser	Ile	Ile	Asn	Trp	His	Leu	Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	
			490			495							500			
ttt	aag	gaa	gtc	ggg	tat	tac	aa	c	gtc	tat	gcc	aag	aag	gga	gaa	1588
Phe	Lys	Glu	Val	Gly	Tyr	Tyr	Asn	Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	
			505			510							515			520
ctc	tcc	atc	aac	gag	gag	aaa	atc	ctg	tgg	agt	ggg	ttc	tcc	agg	gag	1636
Leu	Phe	Ile	Asn	Glu	Glu	Lys	Ile	Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	
			525			530							535			
gtg	ccc	tcc	aac	tgc	agc	cga	gac	tgc	ctg	gca	ggg	acc	agg	aaa		1684
Val	Pro	Phe	Ser	Asn	Cys	Ser	Arg	Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	
			540			545							550			
ggg	atc	att	gag	ggg	gag	ccc	acc	tgc	tgc	ttt	gag	tgt	gtg	gag	tgt	1732
Gly	Ile	Ile	Glu	Gly	Glu	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	
			555			560							565			
cct	gat	ggg	gag	tat	agt	gat	gag	aca	gat	gcc	agt	gcc	tgt	aac	aag	1780
Pro	Asp	Gly	Glu	Tyr	Ser	Asp	Glu	Thr	Asp	Ala	Ser	Ala	Cys	Asn	Lys	
			570			575							580			
tgc	cca	gat	gac	ttc	tgg	tcc	aat	gag	aac	cac	acc	tcc	tgc	att	gcc	1828
Cys	Pro	Asp	Asp	Phe	Trp	Ser	Asn	Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	
			585			590							595			600
aag	gag	atc	gag	ttt	ctg	tcg	tgg	acg	gag	ccc	ttt	ggg	atc	gca	ctc	1876
Lys	Glu	Ile	Glu	Phe	Leu	Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	
			605			610							615			

THE HUMAN GROWTH HORMONE

acc ctc ttt gcc qtg ctg ggc att ttc ctg aca gcc ttt gtg ctg ggt		1924
Thr Leu Phe Ala Val Leu Gly Ile Phe Leu Thr Ala Phe Val Leu Gly		
620	625	630
gtg ttt atc aag ttc cgc aac aca ccc att gtc aag gcc acc aac cga		1972
Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg		
635	640	645
gag ctc tcc tac ctc ctc ttc tcc ctg ctc tgc tgc ttc tcc agc		2020
Glu Leu Ser Tyr Leu Leu Phe Ser Leu Leu Cys Cys Phe Ser Ser		
650	655	660
tcc ctg ttc atc ggg gag ccc cag gac tgg acg tgc cgc ctg cgc		2068
Ser Leu Phe Phe Ile Gly Glu Pro Gln Asp Trp Thr Cys Arg Leu Arg		
665	670	675
cag ccg gcc ttt qgc atc agc ttc gtg ctc tgc atc tca tgc atc ctg		2116
Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu		
685	690	695
gtg aaa acc aac cgt gtc ctc ctg gtg ttt gag gcc aag atc ccc acc		2164
Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr		
700	705	710
agc ttc cac cgc aag tgg tgg ggg ctc aac ctg cag ttc ctg ctg gtt		2212
Ser Phe His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val		
715	720	725
ttc ctc tgc acc ttc atg cag att gtc atc tgt gtg atc tgg ctc tac		2260
Phe Leu Cys Thr Phe Met Gln Ile Val Ile Cys Val Ile Trp Leu Tyr		
730	735	740
acc gcg ccc ccc tca agc tac cgc aac cag gag ctg gag gag atc		2308
Thr Ala Pro Pro Ser Ser Tyr Arg Asn Gln Glu Leu Glu Asp Glu Ile		
745	750	755
760		
atc ttc atc acg tgc cac gag ggc tcc ctc atg gcc ctg ggc ttc ctg		2356
Ile Phe Ile Thr Cys His Glu Gly Ser Leu Met Ala Leu Gly Phe Leu		
765	770	775
atc ggc tac acc tgc ctg gct gcc atc tgc ttc ttc ttt gcc ttc		2404
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Ala Phe		
780	785	790
aag tcc cgg aag ctg cgc gag aac ttc aat gaa gcc aag ttc atc acc		2452
Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile Thr		
795	800	805
ttc agc atg ctc atc ttc atc gtc tgg atc tcc ttc att cca gcc		2500
Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala		
810	815	820
tat gcc agc acc tat ggc aag ttt gtc tct gcc gta gag gtg att gcc		2548
Tyr Ala Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala		
825	830	835
840		
atc ctg gca gcc agc ttt ggc ttg ctg gcg tgc atc ttc ttc aac aag		2596
Ile Leu Ala Ala Ser Phe Gly Leu Leu Ala Cys Ile Phe Phe Asn Lys		
845	850	855
acc tac atc att ctc ttc aag cca tcc cgc aac acc atc gag gag gtg		2644

1000 BASE PAIR

Thr Tyr Ile Ile Leu Phe Lys Pro Ser Arg Asn Thr Ile Glu Glu Val  
860 865 870

cgt tgc agc acc gca cgt cac gct ttc aag gtg gct gcc cgg gcc acg 2692  
Arg Cys Ser Thr Ala Arg His Ala Phe Lys Val Ala Ala Arg Ala Thr  
875 880 885

ctg cgc cgc agc aac gtc tcc cgc aag cgg tcc agc agc ctt gga ggc 2740  
Leu Arg Arg Ser Asn Val Ser Arg Lys Arg Ser Ser Ser Leu Gly Gly  
890 895 900

tcc acg gga tcc acc ccc tcc tcc atc agc agc aag agc aac agc 2788  
Ser Thr Gly Ser Thr Pro Ser Ser Ser Ile Ser Ser Lys Ser Asn Ser  
905 910 915 920

gaa gac cca ttc cca cag ccc gag agg cag aag cag cag cag ccg ctg 2836  
Glu Asp Pro Phe Pro Gln Pro Glu Arg Gln Lys Gln Gln Gln Pro Leu  
925 930 935

gcc cta acc cag caa gag cag cag cag ccc ctg acc ctc cca cag 2884  
Ala Leu Thr Gln Gln Glu Gln Gln Gln Pro Leu Thr Leu Pro Gln  
940 945 950

cag caa cga tct cag cag cag ccc aga tgc aag cag aag gtc atc ttt 2932  
Gln Gln Arg Ser Gln Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe  
955 960 965

ggc agc ggc acg gtc acc ttc tca ctg agc ttt gat gag cct cag aag 2980  
Gly Ser Gly Thr Val Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys  
970 975 980

aac gcc atg gcc cac agg aat tct acg cac cag aac tcc ctg gag gcc 3028  
Asn Ala Met Ala His Arg Asn Ser Thr His Gln Asn Ser Leu Glu Ala  
985 990 995 1000

cag aaa agc agc gat acg ctg acc cga cac cag cca tta ctc ccg ctg 3076  
Gln Lys Ser Ser Asp Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu  
1005 1010 1015

cag tgc ggg gaa acg gac tta gat ctg acc gtc cag gaa aca ggt ctg 3124  
Gln Cys Gly Glu Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu  
1020 1025 1030

caa gga cct gtg ggt gga gac cag cgg cca gag gtg gag gac cct gaa 3172  
Gln Gly Pro Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu  
1035 1040 1045

gag ttg tcc cca gca ctt gta gtg tcc agt tca cag agc ttt gtc atc 3220  
Glu Leu Ser Pro Ala Leu Val Val Ser Ser Gln Ser Phe Val Ile  
1050 1055 1060

agt ggt gga ggc agc act gtt aca gaa aac gta gtg aat tca 3262  
Ser Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser  
065 1070 1075

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gatgaggaat cgccccagac tccttcctc tgaggaaga 3361

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20 25 30  
Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp  
35 40 45  
Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn  
50 55 60  
Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu  
65 70 75 80  
Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg  
85 90 95  
Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu  
100 105 110  
Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe  
115 120 125  
Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala  
130 135 140  
Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe  
145 150 155 160  
Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Arg Leu Leu Ser Asn  
165 170 175  
Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His  
180 185 190  
Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp  
195 200 205  
Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu  
210 215 220  
Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser  
225 230 235 240  
Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Ile Gln His Val Val  
245 250 255  
Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser  
260 265 270  
Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile  
275 280 285  
Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu  
290 295 300  
Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe  
305 310 315 320  
Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys  
325 330 335  
Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp  
340 345 350  
Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu  
355 360 365  
Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe  
370 375 380  
Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn  
385 390 395 400  
Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile  
405 410 415  
Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln  
420 425 430  
Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser

435                          440                          445  
Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu  
450                          455                          460  
Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp  
465                          470                          475                          480  
Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu  
485                          490                          495  
Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn  
500                          505                          510  
Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile  
515                          520                          525  
Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg  
530                          535                          540  
Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr  
545                          550                          555                          560  
Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu  
565                          570                          575  
Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn  
580                          585                          590  
Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp  
595                          600                          605  
Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile  
610                          615                          620  
Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr  
625                          630                          635                          640  
Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Phe  
645                          650                          655  
Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro  
660                          665                          670  
Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe  
675                          680                          685  
Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu  
690                          695                          700  
Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly  
705                          710                          715                          720  
Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile  
725                          730                          735  
Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg  
740                          745                          750  
Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly  
755                          760                          765  
Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala  
770                          775                          780  
Ala Ile Cys Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn  
785                          790                          795                          800  
Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile  
805                          810                          815  
Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe  
820                          825                          830  
Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu  
835                          840                          845  
Leu Ala Cys Ile Phe Phe Asn Lys Thr Tyr Ile Ile Leu Phe Lys Pro  
850                          855                          860  
Ser Arg Asn Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Arg His Ala  
865                          870                          875                          880  
Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg  
885                          890                          895  
Lys Arg Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser  
900                          905                          910  
Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu  
915                          920                          925  
Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln

930                    935                    940  
Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro  
945                    950                    955                    960  
Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser  
965                    970                    975  
Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn Ser  
980                    985                    990  
Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr  
995                    1000                    1005  
Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu Asp  
1010                    1015                    1020  
Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly Asp Gln  
1025                    1030                    1035                    104  
Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala Leu Val Val  
1045                    1050                    1055  
Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly Ser Thr Val Thr  
1060                    1065                    1070  
Glu Asn Val Val Asn Ser  
1075

STRUCTURE OF RIBOSOME